Pending clims in U.S. Patent Application No. 09/899,302

24. (new) A polynucleic acid specifically hybridizing with a sequence selected from the group consisting of SEQ ID NO: 55 to SEQ ID NO: 81, under conditions allowing discrimination of up to 1 nucleotide mismatch, or the complement thereof.

25. (new) An HCV virus characterized by any of the 5' UTR nucleotide sequences selected from the group consisting of SEQ ID NO: 55 to 81.

Pending clims in U.S. Patent Application No. 09/899,044

24. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample on the basis of the presence of a genotype-specific sequence or an isolate-specific mutation present in any of SEQ ID NO 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80 or 81.

25. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample on the basis of the presence of any of SEQ ID NO 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80 or 81.

26. (new) The method according to claim 24 or 25, wherein said method comprises the determination of the presence of said genotype-specific sequence or isolate-specific mutation of any of SEQ ID NO 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80 or 81 by means of a sequencing reaction.

27. (new) A method comprising the determination of the presence in a biological sample of at least one of the following variable nucleotide regions or positions of any HCV 5'UTR sequence by means of a sequencing reaction, wherein said method detects the nucleotide variation present between HCV strains in at least one of the following regions of HCV:

(a) the type-specific variable region between positions –170 and –155,

(b) the type-specific variable region between positions –132 and -117, and/or,

(c) the type-specific variable region between positions –291 and -55.

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28. (new) The method according to claim 27 wherein said method comprises the determination of said nucleotide variations present in said regions of any of SEQ ID NO 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80 or 81.

29. (new) An HCV genotyping method comprising the steps of a method according to claim 24.

30. (new) An HCV genotyping method comprising the steps of a method according to claim 25.

31. (new) An HCV genotyping method comprising the steps of a method according to claim 26.

32. (new) An HCV genotyping method comprising the steps of a method according to claim 27.

33. (new) An HCV genotyping method comprising the steps of a method according to claim 28.

34. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample on the basis of the presence of a genotype-specific sequence or an isolate-specific mutation present in a nucleic acid encoding any of SEQ ID NOs 82, 83, 84, 85, 86, 87, 88, 89, 90, 91 or 92.

35. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample on the basis of the presence of a nucleotide sequence encoding any of SEQ ID NOs 82, 83, 84, 85, 86, 87, 88, 89, 90, 91 or 92.

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36. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample on the basis of the presence of at least part of an amino acid sequence of any of SEQ ID NOs 82, 83, 84, 85, 86, 87, 88, 89, 90, 91 or 92.

37. (new) A method according to claim 34 or 35 wherein said method comprises the determination of the presence of said genotype-specific sequence or isolate-specific mutation by means of a sequencing reaction.

38. (new) An HCV genotyping method comprising the steps of the method according to claim 34.

39. (new) An HCV genotyping method comprising the steps of the method according to claim 35.

40. (new) An HCV genotyping method comprising the steps of the method according to claim 36.

41. (new) An HCV genotyping method comprising the steps of the method according to claim 37.

42. (new) A method according to any of claims 24, 25, 27-30, 32-36 or 38-40 wherein at least one primer is used.

43. (new) A method according to claim 26 wherein at least one primer is used.

44. (new) A method according to claim 31 wherein at least one primer is used.

45. (new) A method according to claim 37 wherein at least one primer is used.

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Pending clims in U.S. Patent Application No. 09/378,900

29. (Twice Amended) A polynucleic acid consisting of 15 to 50 nucleotides which specifically hybridizes with at least one sequence selected from the group consisting of

TCT AGC CAT GGC GTT AGT RYG AGT GT (SEQ ID NO: 3),

CCG CGA GAC TGC TAG C (SEQ ID NO: 7),

TTA CCG GGA AGA CTG G (SEQ ID NO: 11),

TTT CTG GGT ATT GAG C (SEQ ID NO: 14),

TCT TGG AGC AAC CCG C (SEQ ID NO: 15),

AAT YGC CGG GAT GAC C (SEQ ID NO: 17),

TTC TTG GAA CTA ACC C (SEQ ID NO: 18),

TTT CCG GGC ATT GAG C (SEQ ID NO: 19),

CCG CGA GAT CAC TAG C (SEQ ID NO: 21),

CCG GGA AGA CTG GGT C (SEQ ID NO: 22),

ATA GAG TGG GTT TAT C (SEQ ID NO: 26),

wherein Y is T or C,

K is G or T, and

R is G or A, or the complement thereof,

and the corresponding sequences wherein T had been replaced by U.

30. (Twice Amended) A polynucleic acid consisting of a polynucleic acid sequence selected from the group consisting of

TCT AGC CAT GGC GTT AGT RYG AGT GT (SEQ ID NO: 3),

AAT TGC CAG GAC GAC C (SEQ ID NO: 5),

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TCT CCA GGC ATT GAG C (SEQ ID NO: 6),

CCG CGA GAC TGC TAG C (SEQ ID NO: 7),

TAG CGT TGG GTT GCG A (SEQ ID NO: 8),

TTR CCG GRA AGA CTG G (SEQ ID NO: 9),

TGR CCG GGC ATA GAG T (SEQ ID NO: 10),

TTA CCG GGA AGA CTG G (SEQ ID NO: 11),

TGA CCG GAC ATA GAG T (SEQ ID NO: 12),

AAT CGC TGG GGT GAC C (SEQ ID NO: 13),

TTT CTG GGT ATT GAG C (SEQ ID NO: 14),

TCT TGG AGC AAC CCG C (SEQ ID NO: 15),

TCT TGG AAC AAC CCG C (SEQ ID NO: 16),

AAT YGC CGG GAT GAC C (SEQ ID NO: 17),

TTC TTG GAA CTA ACC C (SEQ ID NO: 18),

TTT CCG GGC ATT GAG C (SEQ ID NO: 19),

TTG GGC GYG CCC CGG C (SEQ ID NO: 20),

CCG CGA GAT CAC TAG C (SEQ ID NO: 21),

CCG GGA AGA CTG GGT C (SEQ ID NO: 22),

CCG GAA AGA CTG GGT C (SEQ ID NO: 23),

ACC CAC TCT ATG CCC G (SEQ ID NO: 24),

ACC CAC TCT ATG TCC G (SEQ ID NO: 25),

ATA GAG TGG GTT TAT C (SEQ ID NO: 26), and

TCT GCG GAA CCG GTG A (SEQ ID NO: 27),

wherein Y is T or C,

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K is G or T, and

R is G or A, or the complement of said polynucleic acid sequence.

31. A polynucleic acid consisting of 15 to 50 nucleotides which specifically hybridizes with at least one sequence selected from the group consisting of

CCC CGC AAG ACT GCT A (SEQ ID NO: 31),

CGT ACA GCC TCC AGG C (SEQ ID NO: 32),

GGA CCC AGT CTT CCT G (SEQ ID NO: 33),

TGC CTG GTC ATT TGG G (SEQ ID NO: 34),

TKT CTG GGT ATT GAG C (SEQ ID NO: 35),

CCG CAA GAT CAC TAG C (SEQ ID NO: 36),

GAG TGT TGT ACA GCC T (SEQ ID NO: 37),

AAT CGC CGG GAT GAC C (SEQ ID NO: 38),

GAG TGT TGT GCA GCC T (SEQ ID NO: 39),

AAT CGC CGG GAC GAC C (SEQ ID NO: 40),

AAT GCC CGG CAA TTT G (SEQ ID NO: 41),

AAT CGC CGA GAT GAC C (SEQ ID NO: 42),

AAT GCT CGG AAA TTT G (SEQ ID NO: 43),

GAG TGT CGA ACA GCC T (SEQ ID NO: 44),

AAT TGC CGG GAT GAC C (SEQ ID NO: 45),

GGG TCC TTT CCA TTG G (SEQ ID NO: 48),

AAT CGC CAG GAT GAC C (SEQ ID NO: 49),

TGC CTG GAA ATT TGG G (SEQ ID NO: 50),

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GAG TGT CGT ACA GCC T (SEQ ID NO: 51),

AGT YCA CCG GAA TCG C (SEQ ID NO: 52),

GGA ATC GCC AGG ACG A (SEQ ID NO: 53),

GAA TCG CCG GGT TGA C (SEQ ID NO: 54),

wherein Y is T or C,

K is G or T, and

R is G or A, or the complement thereof,

and the corresponding sequence wherein T had been replaced by U.

32. A polynucleic acid consisting of a polynucleic acid sequence selected from the group consisting of

AAT TGC CAG GAY GAC C (SEQ ID NO: 28),

GCT CAG TGC CTG GAG A (SEQ ID NO: 29),

CCG CGA GAC YGC TAG C (SEQ ID NO: 30),

CCC CGC AAG ACT GCT A (SEQ ID NO: 31),

CGT ACA GCC TCC AGG C (SEQ ID NO: 32),

GGA CCC AGT CTT CCT G (SEQ ID NO: 33),

TGC CTG GTC ATT TGG G (SEQ ID NO: 34),

TKT CTG GGT ATT GAG C (SEQ ID NO: 35),

CCG CAA GAT CAC TAG C (SEQ ID NO: 36),

GAG TGT TGT ACA GCC T (SEQ ID NO: 37),

AAT CGC CGG GAT GAC C (SEQ ID NO: 38),

GAG TGT TGT GCA GCC T (SEQ ID NO: 39),

AAT CGC CGG GAC GAC C (SEQ ID NO: 40),

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AAT GCC CGG CAA TTT G (SEQ ID NO: 41),

AAT CGC CGA GAT GAC C (SEQ ID NO: 42),

AAT GCT CGG AAA TTT G (SEQ ID NO: 43),

GAG TGT CGA ACA GCC T (SEQ ID NO: 44),

AAT TGC CGG GAT GAC C (SEQ ID NO: 45),

TCT CCG GGC ATT GAG C (SEQ ID NO: 46),

AAT TGC CGG GAC GAC C (SEQ ID NO: 47),

GGG TCC TTT CCA TTG G (SEQ ID NO: 48),

AAT CGC CAG GAT GAC C (SEQ ID NO: 49),

TGC CTG GAA ATT TGG G (SEQ ID NO: 50),

GAG TGT CGT ACA GCC T (SEQ ID NO: 51),

AGT YCA CCG GAA TCG C (SEQ ID NO: 52),

GGA ATC GCC AGG ACG A (SEQ ID NO: 53), and

GAA TCG CCG GGT TGA C (SEQ ID NO: 54),

wherein Y is T or C,

K is G or T, and

R is G or A, or the complement of said polynucleic acid sequence.

33. (Amended) A polynucleic acid consisting of 15 to 50 nucleotides which specifically hybridizes with at least one sequence selected from the group consisting of

GAG TGT TGT ACA GCC TCC (SEQ ID NO: 93),

TGC CCG GAA ATT TGG GC (SEQ ID NO: 94),

TGC CCG GAG ATT TGG G (SEQ ID NO: 95),

GAG TGT CGA ACA GCC TC (SEQ ID NO: 96), and

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the corresponding sequence wherein T had been replaced by U.

34. A polynucleic acid consisting of the polynucleic acid sequence selected from the group consisting of

GAG TGT TGT ACA GCC TCC (SEQ ID NO: 93),

TGC CCG GAA ATT TGG GC (SEQ ID NO: 94),

TGC CCG GAG ATT TGG G (SEQ ID NO: 95), and

GAG TGT CGA ACA GCC TC (SEQ ID NO: 96),

or the complement of said polynucleic acid sequence.

36. A polynucleic acid consisting of the polynucleic acid sequence selected from the group consisting of SEQ ID NO: 55 to SEQ ID NO: 81 or the complement of said polynucleic acid sequence